RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/594,117
Source: IFW P
Date Processed by STIC: 10/06/2006

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IFWP

RAW SEQUENCE LISTING DATE: 10/06/2006
PATENT APPLICATION: **US/10/594,117** TIME: 11:10:29

Input Set : **A:\004974.01219 sequence listing.txt**
Output Set: **N:\CRF4\10062006\J594117.raw**

3 <110> APPLICANT: Golz, Stefan
4 Bruggemeier, Ulf
5 Geerts, Andreas
6 Summer, Holger
8 <120> TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with Protein
9 Kinase, cGMP-Dependent, Type I (PRKG1)
11 <130> FILE REFERENCE: 004974.01219
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/594,117
C--> 12 <141> CURRENT FILING DATE: 2006-09-25
12 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/02531
13 <151> PRIOR FILING DATE: 2005-03-10
15 <150> PRIOR APPLICATION NUMBER: EP 04007085.6
16 <151> PRIOR FILING DATE: 2004-03-24
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3740
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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29 gggcaccttg cgggatttac agtacgcgct ccaggagaag atcgaggagc tgaggcagcg 120
30 ggatgctctc atcgacgagc tggagctgga gttggatcag aaggacgaac tgatccagaa 180
31 gctgcagaac gagctggaca agtaccgctc ggtgatccga ccagccaccc agcaggcgca 240
32 gaagcagagc gcgagcacct tgcagggcga gccgcgcacc aagcggcagg cgatctccgc 300
33 cgagcccacc gccttcgaca tccaggatct cagccatgtg accctgccct tctaccccaa 360
34 gagcccacag tccaaggatc ttataaagga agctatcctt gacaatgact ttatgaagaa 420
35 cttggagctg tcgcagatcc aggagattgt ggattgtatg tacccggtgg agtatggcaa 480
36 ggacagttgc atcatcaaag aaggagacgt ggggtcactg gtgtatgtca tggaagatgg 540
37 taaggttgaa gttacaaaag aaggtgtgaa gttgtgtacc atgggtccag gaaaagtgtt 600
38 tggggaattg gctattcttt acaactgtac ccggacagcg accgtcaaga ctcttgtaaa 660
39 tgtaaaactc tgggccattg atcgacaatg ttttcaaaca ataatgatga ggacaggact 720
40 catcaagcat accgagtata tggaattttt aaaaagcgtt ccaacattcc agagccttcc 780
41 tgaagagatc ctcagcaagc ttgctgatgt ccttgaagag acccactatg aaaatggaga 840
42 atatattatc aggcaaggtg caagagggga caccttcttt atcatcagca aaggaacggt 900
43 aaatgtcact cgtgaagact caccgagtga agacccagtc tttcttagaa ctttaggaaa 960
44 aggagactgg tttggagaga aagccttgca gggggaagat gtgagaacag caaacgtaat 1020
45 tgctgcagaa gctgtaacct gccttgtgat tgacagagac tcttttaaac atttgattgg 1080
46 agggctggat gatgtttcta ataaagcata tgaagatgca gaagctaaag caaaatatga 1140
47 agctgaagcg gctttcttcg ccaacctgaa gctgtctgat ttcaacatca ttgataccct 1200
48 tggagttgga ggtttcggac gagtagaact ggtccagttg aaaagtgaag aatccaaaac 1260
49 gtttgcaatg aagattctca agaaacgtca cattgtggac acaagacagc aggagcacat 1320
50 ccgctcagag aagcagatca tgcaggggc tcattccgat ttcatagtga gactgtacag 1380

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 51 aacatttaag gacagcaaat atttgtatat gttgatggaa gcttgtctag gtggagagct   1440
 52 ctggaccatt ctcagggata gaggttcgtt tgaagattct acaaccagat tttacacagc   1500
 53 atgtgtggta gaagcttttg cctatctgca ttccaaagga atcatttaca gggacctcaa   1560
 54 gccagaaaat ctcatcctag atcaccgagg ttatgccaaa ctggttgatt ttggctttgc   1620
 55 aaagaaaata ggatttggaa agaaaacatg gacttttttgt gggactccag agtatgtagc  1680
 56 cccagagatc atcctgaaca aaggccatga catttcagcc gactactggt cactgggaat   1740
 57 cctaatgtat gaactcctga ctggcagccc acctttctca ggcccagatc ctatgaaaac   1800
 58 ctataacatc atattgaggg ggattgacat gatagaattt ccaaagaaga ttgccaaaaa   1860
 59 tgctgctaat ttaattaaaa aactatgcag ggacaatcca tcagaaagat tagggaattt   1920
 60 gaaaaatgga gtaaaagaca ttcaaaagca caaatggttt gagggcttta actgggaagg   1980
 61 cttaagaaaa ggtaccttga cacctcctat aataccaagt gttgcatcac ccacagacac   2040
 62 aagtaatttt gacagtttcc ctgaggacaa cgatgaacca ccacctgatg acaactcagg   2100
 63 atgggatata gacttctaat gtatttctct tacctgcttc tgccttgctg aagacagctt   2160
 64 tttctgagac acagctgcca gcaaacctga gggaaagaga gaagattagt gctcggggtc   2220
 65 accatgatgc ctttgatcga tgctgctcca gtaactacag tggcattagg acttatcgct   2280
 66 tagatgacaa tagtgctctt tacatgtttt ctgtttgaac ctaaaatagc agttgacatg   2340
 67 gtggtcctga agcaaagcct ttcaccagta aagagatgtt ttctattgtt gcaatgacct   2400
 68 tgctttgctc tgattataat ttgaaagact gtaggaaaca cttcaatgta gtataagagt   2460
 69 ctgtaccttg ctggaatatt caagaagatg aaagaataat atattgggta caatagatta   2520
 70 ctatggtaca gaaactgggc tattcccttt cttcaagtga aggctgtggg atctattaca   2580
 71 gctgcaggcc ggtgtatata ccatacaaaa gaggaccaca catctgttgg tcacagagtt   2640
 72 catgtcacac cagtgctaga agtttcatga ttttatttcc cagcagtgct gatgacaaga   2700
 73 ctgaatgtta ccttttcttt ctgacagatt ttaaaaattg atatgataaa agcacaactg   2760
 74 ctatagattc tgctgagacc tctcatagta ggtatatatg agttttcaca gaagactgaa   2820
 75 aaataatgca tgatatttgt ttgtttttt tgataaattg gcatgacaga gtggggaaaa   2880
 76 aaagcaattc acaaaaccat ttcatatttt ttaaaatatt gtgcttaaag atggtcctgg   2940
 77 aagtaaatga ctagcagcca attggtttta cttaacatac cctcaaactg aggcttaaag   3000
 78 tattcccttt tataaaaata aatgcttggg gtagggtgga gtggggaggg attaaaaccc   3060
 79 atccaaaaaa taaataaaaa ctatataggt gctatgtata tctttcatct gtaaatgtca   3120
 80 gtgtctgaac agcaacacaa attcaaatca ttatacgtgt agccagaaac tcaagcattt   3180
 81 tcactaaagt tattaaacca aactcctgtc caatttgact tatacaacat agtcagtcta   3240
 82 gagttgagag acaaaggtaa ttataaacct atttgaacta gcttcttgtc ttaggcctga   3300
 83 accaaaaaac aacaaacaaa caaaaaacaa gaatgaaaaa cagaaataaa agaagtagaa   3360
 84 aagacaaaga aagaaagccc aaagtcaaag ttgttaatat ttacaggttt accagatctg   3420
 85 gaacattact tatttgaggt cagagaacaa aacaagaacc tggccaggtg ttgattacct   3480
 86 tttagtgaat aagctgagtc catatacttg tctaactaag aaagcagtac agaggaaaac   3540
 87 aggaacctga ttttttaaa ataaatttta aataaaatag aattactaca attctgcaat   3600
 88 ttcatactac ctaaaaaaga ctagatttga aaatgtcaag ctgatttact ttattcacat   3660
 89 ggagaaaaga atccacaaat taaactgagt ccttcactgg catgccagtt gactattatt   3720
 90 agctgtcata agtaaccccg                                             3740
 92 <210> SEQ ID NO: 2
 93 <211> LENGTH: 686
 94 <212> TYPE: PRT
 95 <213> ORGANISM: Homo sapiens
 97 <400> SEQUENCE: 2
 98 Met Gly Thr Leu Arg Asp Leu Gln Tyr Ala Leu Gln Glu Lys Ile Glu
 99 1               5                  10                  15
100 Glu Leu Arg Gln Arg Asp Ala Leu Ile Asp Glu Leu Glu Leu Glu Leu
101             20                  25                  30
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102 Asp Gln Lys Asp Glu Leu Ile Gln Lys Leu Gln Asn Glu Leu Asp Lys
103         35                  40                  45
104 Tyr Arg Ser Val Ile Arg Pro Ala Thr Gln Gln Ala Gln Lys Gln Ser
105     50                  55                  60
106 Ala Ser Thr Leu Gln Gly Glu Pro Arg Thr Lys Arg Gln Ala Ile Ser
107 65                  70                  75                  80
108 Ala Glu Pro Thr Ala Phe Asp Ile Gln Asp Leu Ser His Val Thr Leu
109                 85                  90                  95
110 Pro Phe Tyr Pro Lys Ser Pro Gln Ser Lys Asp Leu Ile Lys Glu Ala
111             100                 105                 110
112 Ile Leu Asp Asn Asp Phe Met Lys Asn Leu Glu Leu Ser Gln Ile Gln
113         115                 120                 125
114 Glu Ile Val Asp Cys Met Tyr Pro Val Glu Tyr Gly Lys Asp Ser Cys
115     130                 135                 140
116 Ile Ile Lys Glu Gly Asp Val Gly Ser Leu Val Tyr Val Met Glu Asp
117 145                 150                 155                 160
118 Gly Lys Val Glu Val Thr Lys Glu Gly Val Lys Leu Cys Thr Met Gly
119                 165                 170                 175
120 Pro Gly Lys Val Phe Gly Glu Leu Ala Ile Leu Tyr Asn Cys Thr Arg
121             180                 185                 190
122 Thr Ala Thr Val Lys Thr Leu Val Asn Val Lys Leu Trp Ala Ile Asp
123         195                 200                 205
124 Arg Gln Cys Phe Gln Thr Ile Met Met Arg Thr Gly Leu Ile Lys His
125     210                 215                 220
126 Thr Glu Tyr Met Glu Phe Leu Lys Ser Val Pro Thr Phe Gln Ser Leu
127 225                 230                 235                 240
128 Pro Glu Glu Ile Leu Ser Lys Leu Ala Asp Val Leu Glu Glu Thr His
129                 245                 250                 255
130 Tyr Glu Asn Gly Glu Tyr Ile Ile Arg Gln Gly Ala Arg Gly Asp Thr
131             260                 265                 270
132 Phe Phe Ile Ile Ser Lys Gly Thr Val Asn Val Thr Arg Glu Asp Ser
133         275                 280                 285
134 Pro Ser Glu Asp Pro Val Phe Leu Arg Thr Leu Gly Lys Gly Asp Trp
135     290                 295                 300
136 Phe Gly Glu Lys Ala Leu Gln Gly Glu Asp Val Arg Thr Ala Asn Val
137 305                 310                 315                 320
138 Ile Ala Ala Glu Ala Val Thr Cys Leu Val Ile Asp Arg Asp Ser Phe
139                 325                 330                 335
140 Lys His Leu Ile Gly Gly Leu Asp Asp Val Ser Asn Lys Ala Tyr Glu
141             340                 345                 350
142 Asp Ala Glu Ala Lys Ala Lys Tyr Glu Ala Glu Ala Ala Phe Phe Ala
143         355                 360                 365
144 Asn Leu Lys Leu Ser Asp Phe Asn Ile Ile Asp Thr Leu Gly Val Gly
145     370                 375                 380
146 Gly Phe Gly Arg Val Glu Leu Val Gln Leu Lys Ser Glu Glu Ser Lys
147 385                 390                 395                 400
148 Thr Phe Ala Met Lys Ile Leu Lys Lys Arg His Ile Val Asp Thr Arg
149                 405                 410                 415
150 Gln Gln Glu His Ile Arg Ser Glu Lys Gln Ile Met Gln Gly Ala His
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```
151             420                 425                 430
152 Ser Asp Phe Ile Val Arg Leu Tyr Arg Thr Phe Lys Asp Ser Lys Tyr
153         435                 440                 445
154 Leu Tyr Met Leu Met Glu Ala Cys Leu Gly Gly Glu Leu Trp Thr Ile
155     450                 455                 460
156 Leu Arg Asp Arg Gly Ser Phe Glu Asp Ser Thr Thr Arg Phe Tyr Thr
157 465                 470                 475                 480
158 Ala Cys Val Val Glu Ala Phe Ala Tyr Leu His Ser Lys Gly Ile Ile
159                 485                 490                 495
160 Tyr Arg Asp Leu Lys Pro Glu Asn Leu Ile Leu Asp His Arg Gly Tyr
161             500                 505                 510
162 Ala Lys Leu Val Asp Phe Gly Phe Ala Lys Lys Ile Gly Phe Gly Lys
163         515                 520                 525
164 Lys Thr Trp Thr Phe Cys Gly Thr Pro Glu Tyr Val Ala Pro Glu Ile
165     530                 535                 540
166 Ile Leu Asn Lys Gly His Asp Ile Ser Ala Asp Tyr Trp Ser Leu Gly
167 545                 550                 555                 560
168 Ile Leu Met Tyr Glu Leu Leu Thr Gly Ser Pro Pro Phe Ser Gly Pro
169                 565                 570                 575
170 Asp Pro Met Lys Thr Tyr Asn Ile Ile Leu Arg Gly Ile Asp Met Ile
171             580                 585                 590
172 Glu Phe Pro Lys Lys Ile Ala Lys Asn Ala Ala Asn Leu Ile Lys Lys
173         595                 600                 605
174 Leu Cys Arg Asp Asn Pro Ser Glu Arg Leu Gly Asn Leu Lys Asn Gly
175     610                 615                 620
176 Val Lys Asp Ile Gln Lys His Lys Trp Phe Glu Gly Phe Asn Trp Glu
177 625                 630                 635                 640
178 Gly Leu Arg Lys Gly Thr Leu Thr Pro Pro Ile Ile Pro Ser Val Ala
179                 645                 650                 655
180 Ser Pro Thr Asp Thr Ser Asn Phe Asp Ser Phe Pro Glu Asp Asn Asp
181             660                 665                 670
182 Glu Pro Pro Pro Asp Asp Asn Ser Gly Trp Asp Ile Asp Phe
183         675                 680                 685
185 <210> SEQ ID NO: 3
186 <211> LENGTH: 20
187 <212> TYPE: DNA
188 <213> ORGANISM: artificial sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: forward primer
193 <400> SEQUENCE: 3
194 agccgactac tggtcactgg                                              20
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 20
198 <212> TYPE: DNA
199 <213> ORGANISM: artificial sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: reverse primer
204 <400> SEQUENCE: 4
205 gatctgggcc tgagaaaggt                                              20
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PATENT APPLICATION: **US/10/594,117** TIME: 11:10:29

Input Set : **A:\004974.01219 sequence listing.txt**
Output Set: **N:\CRF4\10062006\J594117.raw**

207 <210> SEQ ID NO: 5
208 <211> LENGTH: 25
209 <212> TYPE: DNA
210 <213> ORGANISM: artificial sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: probe
215 <400> SEQUENCE: 5
216 tgtatgaact cctgactggc agccc 25

VERIFICATION SUMMARY DATE: 10/06/2006
PATENT APPLICATION: **US/10/594,117** TIME: 11:10:30

Input Set : **A:\004974.01219 sequence listing.txt**
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date